

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Miao, Ningning
Wang, Monica
Mahanthappa, Nagesh K.
Jin, Ping
Pang, Kevin

(ii) TITLE OF INVENTION: Method of Treating Dopaminergic and
GABA-nergic Disorders

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
(B) STREET: ONE POST OFFICE SQUARE
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: AscII (text)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/900,220
(B) FILING DATE: 24-JUL-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: ONV-044.01

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | |
|----|---|-----|
| 5 | ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC | 48 |
| | Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile | |
| | 1 5 10 15 | |
| 10 | TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC | 96 |
| | Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly | |
| | 20 25 30 | |
| 15 | ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG | 144 |
| | Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys | |
| | 35 40 45 | |
| 20 | CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA | 192 |
| | Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg | |
| | 50 55 60 | |
| 25 | TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC | 240 |
| | Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr | |
| | 65 70 75 80 | |
| 30 | CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA | 288 |
| | Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly | |
| | 85 90 95 | |
| 35 | GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG | 336 |
| | Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu | |
| | 100 105 110 | |
| 40 | GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC | 384 |
| | Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr | |
| | 115 120 125 | |
| 45 | GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC | 432 |
| | Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr | |
| | 130 135 140 | |
| 50 | GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG | 480 |
| | Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys | |
| | 145 150 155 160 | |
| 55 | TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC | 528 |
| | Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val | |
| | 165 170 175 | |
| 60 | TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC | 576 |
| | Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn | |
| | 180 185 190 | |
| 65 | TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG | 624 |
| | Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val | |
| | 195 200 205 | |
| 70 | CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG | 672 |
| | His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly | |
| | 210 215 220 | |
| 75 | GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC | 720 |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Asp | Arg | Val | Leu | Ala | Ala | Asp | Ala | Asp | Gly | Arg | Leu | Leu | Tyr | Ser | Asp | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 5 | TTC | CTC | ACC | TTC | CTC | GAC | CGG | ATG | GAC | AGC | TCC | CGA | AAG | CTC | TTC | TAC | 768 |
| | Phe | Leu | Thr | Phe | Leu | Asp | Arg | Met | Asp | Ser | Ser | Arg | Lys | Leu | Phe | Tyr | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 10 | GTC | ATC | GAG | ACG | CGG | CAG | CCC | CGG | GCC | CGG | CTG | CTA | CTG | ACG | GCG | GCC | 816 |
| | Val | Ile | Glu | Thr | Arg | Gln | Pro | Arg | Ala | Arg | Leu | Leu | Leu | Thr | Ala | Ala | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 15 | CAC | CTG | CTC | TTT | GTG | GCC | CCC | CAG | CAC | AAC | CAG | TCG | GAG | GCC | ACA | GGG | 864 |
| | His | Leu | Leu | Phe | Val | Ala | Pro | Gln | His | Asn | Gln | Ser | Glu | Ala | Thr | Gly | |
| | | | | 275 | | | | 280 | | | | | 285 | | | | |
| 20 | TCC | ACC | AGT | GGC | CAG | GCG | CTC | TTC | GCC | AGC | AAC | GTG | AAG | CCT | GGC | CAA | 912 |
| | Ser | Thr | Ser | Gly | Gln | Ala | Leu | Phe | Ala | Ser | Asn | Val | Lys | Pro | Gly | Gln | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 25 | CGT | GTC | TAT | GTG | CTG | GGC | GAG | GGC | GGG | CAG | CAG | CTG | CTG | CCG | GCG | TCT | 960 |
| | Arg | Val | Tyr | Val | Leu | Gly | Glu | Gly | Gly | Gln | Gln | Leu | Leu | Pro | Ala | Ser | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 30 | GTC | CAC | AGC | GTC | TCA | TTG | CGG | GAG | GAG | GCG | TCC | GGA | GCC | TAC | GCC | CCA | 1008 |
| | Val | His | Ser | Val | Ser | Leu | Arg | Glu | Glu | Ala | Ser | Gly | Ala | Tyr | Ala | Pro | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 35 | GTC | ACC | GCC | CAG | GGC | ACC | ATC | CTC | ATC | AAC | CGG | GTG | TTG | GCC | TCC | TGC | 1056 |
| | Leu | Thr | Ala | Gln | Gly | Thr | Ile | Leu | Ile | Asn | Arg | Val | Leu | Ala | Ser | Cys | |
| | | | | 340 | | | | 345 | | | | | | 350 | | | |
| 40 | TAC | GCC | GTC | ATC | GAG | GAG | CAC | AGT | TGG | GCC | CAT | TGG | GCC | TTC | GCA | CCA | 1104 |
| | Tyr | Ala | Val | Ile | Glu | Glu | His | Ser | Trp | Ala | His | Trp | Ala | Phe | Ala | Pro | |
| | | | 355 | | | | | 360 | | | | 365 | | | | | |
| 45 | TTC | CGC | TTG | GCT | CAG | GGG | CTG | CTG | GCC | GCC | CTC | TGC | CCA | GAT | GGG | GCC | 1152 |
| | Phe | Arg | Leu | Ala | Gln | Gly | Leu | Leu | Ala | Ala | Leu | Cys | Pro | Asp | Gly | Ala | |
| | | 370 | | | | 375 | | | | | 380 | | | | | | |
| 50 | ATC | CCT | ACT | GCC | GCC | ACC | ACC | ACC | ACT | GGC | ATC | CAT | TGG | TAC | TCA | CGG | 1200 |
| | Ile | Pro | Thr | Ala | Ala | Thr | Thr | Thr | Thr | Gly | Ile | His | Trp | Tyr | Ser | Arg | |
| | 385 | | | | | 390 | | | | 395 | | | | | | 400 | |
| 55 | CTC | CTC | TAC | CGC | ATC | GGC | AGC | TGG | GTG | CTG | GAT | GGT | GAC | GCG | CTG | CAT | 1248 |
| | Leu | Leu | Tyr | Arg | Ile | Gly | Ser | Trp | Val | Leu | Asp | Gly | Asp | Ala | Leu | His | |
| | | | | 405 | | | | | 410 | | | | | | 415 | | |
| 60 | CCG | CTG | GGC | ATG | GTG | GCA | CCG | GCC | AGC | TG | | | | | | | 1277 |
| | Pro | Leu | Gly | Met | Val | Ala | Pro | Ala | Ser | | | | | | | | |
| | | | | 420 | | | | 425 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | |
|----|---|-----|
| 5 | ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG | 48 |
| | Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu | |
| | 1 5 10 15 | |
| 10 | GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG | 96 |
| | Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg | |
| | 20 25 30 | |
| 15 | CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT | 144 |
| | Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe | |
| | 35 40 45 | |
| 20 | GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG | 192 |
| | Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu | |
| | 50 55 60 | |
| 25 | GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC | 240 |
| | Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn | |
| | 65 70 75 80 | |
| 30 | TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC | 288 |
| | Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp | |
| | 85 90 95 | |
| 35 | CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC | 336 |
| | Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile | |
| | 100 105 110 | |
| 40 | GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC | 384 |
| | Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly | |
| | 115 120 125 | |
| 45 | TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC | 432 |
| | Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly | |
| | 130 135 140 | |
| 50 | CGT GCC TTG GAC ATC ACC ACG TCT GAC CGT GAC CGT AAT AAG TAT GGT | 480 |
| | Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly | |
| | 145 150 155 160 | |
| 55 | TTG TTG GCG CGC CTA GCT GTG GAA GCC GGA TTC GAC TGG GTC TAC TAC | 528 |
| | Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr | |
| | 165 170 175 | |
| 60 | GAG TCC CGC AAC CAC ATC CAC GTA TCG GTC AAA GCT GAT AAC TCA CTG | 576 |
| | Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu | |
| | 180 185 190 | |
| 65 | GCG GTC CGA GCC GGA GGC TGC TTT CCG GGA AAT GCC ACG GTG CGC TTG | 624 |
| | Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu | |
| | 195 200 205 | |
| 70 | CGG AGC GGC GAA CGG AAG GGG CTG AGG GAA CTA CAT CGT GGT GAC TGG | 672 |
| | Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp | |
| | 210 215 220 | |

| | | |
|----|---|------|
| | GTA CTG GCC GCT GAT GCA GCG GGC CGA GTG GTA CCC ACG CCA GTG CTG | 720 |
| | Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu | |
| | 225 230 235 240 | |
| 5 | CTC TTC CTG GAC CGG GAT CTG CAG CGC CGC GCC TCG TTC GTG GCT GTG | 768 |
| | Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val | |
| | 245 250 255 | |
| 10 | GAG ACC GAG CGG CCT CCG CGC AAA CTG TTG CTC ACA CCC TGG CAT CTG | 816 |
| | Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu | |
| | 260 265 270 | |
| 15 | GTG TTC GCT GCT CGC GGG CCA GCG CCT GCT CCA GGT GAC TTT GCA CCG | 864 |
| | Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro | |
| | 275 280 285 | |
| 20 | GTG TTC GCG CGC CGC TTA CGT GCT GGC GAC TCG GTG CTG GCT CCC GGC | 912 |
| | Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly | |
| | 290 295 300 | |
| 25 | GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA | 960 |
| | Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu | |
| | 305 310 315 320 | |
| 30 | GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC | 1008 |
| | Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val | |
| | 325 330 335 | |
| 35 | AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG | 1056 |
| | Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp | |
| | 340 345 350 | |
| 40 | GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT | 1104 |
| | Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala | |
| | 355 360 365 | |
| 45 | CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT | 1152 |
| | Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser | |
| | 370 375 380 | |
| 50 | CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG | 1190 |
| | Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly | |
| | 385 390 395 | |

45 (2) INFORMATION FOR SEQ ID NO:3:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1233

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | ATG | TCT | CCC | GCC | TGG | CTC | CGG | CCC | CGA | CTG | CGG | TTC | TGT | CTG | TTC | CTG | 48 |
| | Met | Ser | Pro | Ala | Trp | Leu | Arg | Pro | Arg | Leu | Arg | Phe | Cys | Leu | Phe | Leu | |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| 5 | CTG | CTG | CTG | CTT | CTG | GTG | CCG | GCG | GCG | CGG | GGC | TGC | GGG | CCG | GGC | CGG | 96 |
| | Leu | Leu | Leu | Leu | Leu | Val | Pro | Ala | Ala | Arg | Gly | Cys | Gly | Pro | Gly | Arg | |
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| 10 | GTG | GTG | GGC | AGC | CGC | CGG | AGG | CCG | CCT | CGC | AAG | CTC | GTG | CCT | CTT | GCC | 144 |
| | Val | Val | Gly | Ser | Arg | Arg | Arg | Pro | Pro | Arg | Lys | Leu | Val | Pro | Leu | Ala | |
| | | | 35 | | | | | 40 | | | | | 45 | | | | |
| 15 | TAC | AAG | CAG | TTC | AGC | CCC | AAC | GTG | CCG | GAG | AAG | ACC | CTG | GGC | GCC | AGC | 192 |
| | Tyr | Lys | Gln | Phe | Ser | Pro | Asn | Val | Pro | Glu | Lys | Thr | Leu | Gly | Ala | Ser | |
| | 50 | | | | | | 55 | | | | | 60 | | | | | |
| 20 | GGG | CGC | TAC | GAA | GGC | AAG | ATC | GCG | CGC | AGC | TCT | GAG | CGC | TTC | AAA | GAG | 240 |
| | Gly | Arg | Tyr | Glu | Gly | Lys | Ile | Ala | Arg | Ser | Ser | Glu | Arg | Phe | Lys | Glu | |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| 25 | CTC | ACC | CCC | AAC | TAC | AAT | CCC | GAC | ATC | ATC | TTC | AAG | GAC | GAG | GAG | AAC | 288 |
| | Leu | Thr | Pro | Asn | Tyr | Asn | Pro | Asp | Ile | Ile | Phe | Lys | Asp | Glu | Glu | Asn | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| 30 | ACG | GGT | GCC | GAC | CGC | CTC | ATG | ACC | CAG | CGC | TGC | AAG | GAC | CGT | CTG | AAC | 336 |
| | Thr | Gly | Ala | Asp | Arg | Leu | Met | Thr | Gln | Arg | Cys | Lys | Asp | Arg | Leu | Asn | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| 35 | TCA | CTG | GCC | ATC | TCT | GTC | ATG | AAC | CAG | TGG | CCT | GGT | GTG | AAA | CTG | CGG | 384 |
| | Ser | Leu | Ala | Ile | Ser | Val | Met | Asn | Gln | Trp | Pro | Gly | Val | Lys | Leu | Arg | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 40 | GTG | ACC | GAA | GGC | CGG | GAT | GAA | GAT | GGC | CAT | CAC | TCA | GAG | GAG | TCT | TTA | 432 |
| | Val | Thr | Glu | Gly | Arg | Asp | Glu | Asp | Gly | His | His | Ser | Glu | Glu | Ser | Leu | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| 45 | CAC | TAT | GAG | GGC | CGC | GCG | GTG | GAT | ATC | ACC | ACC | TCA | GAC | CGT | GAC | CGA | 480 |
| | His | Tyr | Glu | Gly | Arg | Ala | Val | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 50 | AAT | AAG | TAT | GGA | CTG | CTG | GCG | CGC | TTA | GCA | GTG | GAG | GCC | GGC | TTC | GAC | 528 |
| | Asn | Lys | Tyr | Gly | Leu | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | |
| | | | | | 165 | | | | 170 | | | | | | 175 | | |
| 55 | TGG | GTG | TAT | TAC | GAG | TCC | AAG | GCC | CAC | GTG | CAT | TGC | TCT | GTC | AAG | TCT | 576 |
| | Trp | Val | Tyr | Tyr | Glu | Ser | Lys | Ala | His | Val | His | Cys | Ser | Val | Lys | Ser | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 60 | GAG | CAT | TCG | GCC | GCT | GCC | AAG | ACA | GGT | GGC | TGC | TTT | CCT | GCC | GGA | GCC | 624 |
| | Glu | His | Ser | Ala | Ala | Ala | Lys | Thr | Gly | Gly | Cys | Phe | Pro | Ala | Gly | Ala | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 65 | CAG | GTG | CGC | CTA | GAG | AAC | GGG | GAG | CGT | GTG | GCC | CTG | TCA | GCT | GTA | AAG | 672 |
| | Gln | Val | Arg | Leu | Glu | Asn | Gly | Glu | Arg | Val | Ala | Leu | Ser | Ala | Val | Lys | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| 70 | CCA | GGA | GAC | CGG | GTG | CTG | GCC | ATG | GGG | GAG | GAT | GGG | ACC | CCC | ACC | TTC | 720 |
| | Pro | Gly | Asp | Arg | Val | Leu | Ala | Met | Gly | Glu | Asp | Gly | Thr | Pro | Thr | Phe | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 75 | AGT | GAT | GTG | CTT | ATT | TTC | CTG | GAC | CGC | GAG | CCA | AAC | CGG | CTG | AGA | GCT | 768 |

| | | | | | | | | | | | | | | | | | |
|----|------------|------------|----------|------|-----|-----|-----|-----|-----|-----|-----|------------|------------|------|-----|-----|------|
| | Ser | Asp | Val | Leu | Ile | Phe | Leu | Asp | Arg | Glu | Pro | Asn | Arg | Leu | Arg | Ala | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 5 | TTC | CAG | GTC | ATC | GAG | ACT | CAG | GAT | CCT | CCG | CGT | CGG | CTG | GCG | CTC | ACG | 816 |
| | Phe | Gln | Val | Ile | Glu | Thr | Gln | Asp | Pro | Pro | Arg | Arg | Leu | Ala | Leu | Thr | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 10 | CCT | GCC | CAC | CTG | CTC | TTC | ATT | GCG | GAC | AAT | CAT | ACA | GAA | CCA | GCA | GCC | 864 |
| | Pro | Ala | His | Leu | Leu | Phe | Ile | Ala | Asp | Asn | His | Thr | Glu | Pro | Ala | Ala | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 15 | CAC | TTC | CGG | GCC | ACA | TTT | GCC | AGC | CAT | GTG | CAA | CCA | GGC | CAA | TAT | GTG | 912 |
| | His | Phe | Arg | Ala | Thr | Phe | Ala | Ser | His | Val | Gln | Pro | Gly | Gln | Tyr | Val | |
| | | | 290 | | | | 295 | | | | | 300 | | | | | |
| 20 | CTG | GTA | TCA | GGG | GTA | CCA | GGC | CTC | CAG | CCT | GCT | CGG | GTG | GCA | GCT | GTC | 960 |
| | Leu | Val | Ser | Gly | Val | Pro | Gly | Leu | Gln | Pro | Ala | Arg | Val | Ala | Ala | Val | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 25 | TCC | ACC | CAC | GTG | GCC | CTT | GGG | TCC | TAT | GCT | CCT | CTC | ACA | AGG | CAT | GGG | 1008 |
| | Ser | Thr | His | Val | Ala | Leu | Gly | Ser | Tyr | Ala | Pro | Leu | Thr | Arg | His | Gly | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 30 | ACA | CTT | GTG | GTG | GAG | GAT | GTG | GTG | GCC | TCC | TGC | TTT | GCA | GCT | GTG | GCT | 1056 |
| | Thr | Leu | Val | Val | Glu | Asp | Val | Val | Ala | Ser | Cys | Phe | Ala | Ala | Val | Ala | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| 35 | GAC | CAC | CAT | CTG | GCT | CAG | TTG | GCC | TTC | TGG | CCC | CTG | CGA | CTG | TTT | CCC | 1104 |
| | Asp | His | His | Leu | Ala | Gln | Leu | Ala | Phe | Trp | Pro | Leu | Arg | Leu | Phe | Pro | |
| | | | 355 | | | | 360 | | | | | | 365 | | | | |
| 40 | AGT | TTG | GCA | TGG | GGC | AGC | TGG | ACC | CCA | AGT | GAG | GGT | GTT | CAC | TCC | TAC | 1152 |
| | Ser | Leu | Ala | Trp | Gly | Ser | Trp | Thr | Pro | Ser | Glu | Gly | Val | His | Ser | Tyr | |
| | | 370 | | | | 375 | | | | | | 380 | | | | | |
| 45 | CCT | CAG | ATG | CTC | TAC | CGC | CTG | GGG | CGT | CTC | TTG | CTA | GAA | GAG | AGC | ACC | 1200 |
| | Pro | Gln | Met | Leu | Tyr | Arg | Leu | Gly | Arg | Leu | Leu | Leu | Glu | Glu | Ser | Thr | |
| | | | 385 | | | 390 | | | | | 395 | | | | | 400 | |
| 50 | TTC | CAT | CCA | CTG | GGC | ATG | TCT | GGG | GCA | GGA | AGC | TGAAGGGACT | CTAACCACTG | 1253 | | | |
| | Phe | His | Pro | Leu | Gly | Met | Ser | Gly | Ala | Gly | Ser | | | | | | |
| | | | | 405 | | | | | | 410 | | | | | | | |
| 55 | CCCTCCTGGA | ACTGCTGTGC | GTGGATCC | 1281 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1314
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | ATG | CTG | CTG | CTG | CTG | GCC | AGA | TGT | TTT | CTG | GTG | ATC | CTT | GCT | TCC | TCG | 48 |
| | Met | Leu | Leu | Leu | Leu | Ala | Arg | Cys | Phe | Leu | Val | Ile | Leu | Ala | Ser | Ser | |
| 5 | 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | CTG | CTG | GTG | TGC | CCC | GGG | CTG | GCC | TGT | GGG | CCC | GGC | AGG | GGG | TTT | GGA | 96 |
| | Leu | Leu | Val | Cys | Pro | Gly | Leu | Ala | Cys | Gly | Pro | Gly | Arg | Gly | Phe | Gly | |
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| 10 | AAG | AGG | CGG | CAC | CCC | AAA | AAG | CTG | ACC | CCT | TTA | GCC | TAC | AAG | CAG | TTT | 144 |
| | Lys | Arg | Arg | His | Pro | Lys | Lys | Leu | Thr | Pro | Leu | Ala | Tyr | Lys | Gln | Phe | |
| | | | 35 | | | | | 40 | | | | | 45 | | | | |
| 15 | ATT | CCC | AAC | GTA | GCC | GAG | AAG | ACC | CTA | GGG | GCC | AGC | GGC | AGA | TAT | GAA | 192 |
| | Ile | Pro | Asn | Val | Ala | Glu | Lys | Thr | Leu | Gly | Ala | Ser | Gly | Arg | Tyr | Glu | |
| | | 50 | | | | | 55 | | | | | 60 | | | | | |
| 20 | GGG | AAG | ATC | ACA | AGA | AAC | TCC | GAA | CGA | TTT | AAG | GAA | CTC | ACC | CCC | AAT | 240 |
| | Gly | Lys | Ile | Thr | Arg | Asn | Ser | Glu | Arg | Phe | Lys | Glu | Leu | Thr | Pro | Asn | |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| 25 | TAC | AAC | CCC | GAC | ATC | ATA | TTT | AAG | GAT | GAG | GAA | AAC | ACG | GGA | GCA | GAC | 288 |
| | Tyr | Asn | Pro | Asp | Ile | Ile | Phe | Lys | Asp | Glu | Glu | Asn | Thr | Gly | Ala | Asp | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| | CGG | CTG | ATG | ACT | CAG | AGG | TGC | AAA | GAC | AAG | TTA | AAT | GCC | TTG | GCC | ATC | 336 |
| | Arg | Leu | Met | Thr | Gln | Arg | Cys | Lys | Asp | Lys | Leu | Asn | Ala | Leu | Ala | Ile | |
| | | | | 100 | | | | 105 | | | | | 110 | | | | |
| 30 | TCT | GTG | ATG | AAC | CAG | TGG | CCT | GGA | GTG | AGG | CTG | CGA | GTG | ACC | GAG | GGC | 384 |
| | Ser | Val | Met | Asn | Gln | Trp | Pro | Gly | Val | Arg | Leu | Arg | Val | Thr | Glu | Gly | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 35 | TGG | GAT | GAG | GAC | GGC | CAT | CAT | TCA | GAG | GAG | TCT | CTA | CAC | TAT | GAG | GGT | 432 |
| | Trp | Asp | Glu | Asp | Gly | His | His | Ser | Glu | Glu | Ser | Leu | His | Tyr | Glu | Gly | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| 40 | CGA | GCA | GTG | GAC | ATC | ACC | ACG | TCC | GAC | CGG | GAC | CGC | AGC | AAG | TAC | GGC | 480 |
| | Arg | Ala | Val | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | Ser | Lys | Tyr | Gly | |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 45 | ATG | CTG | GCT | CGC | CTG | GCT | GTG | GAA | GCA | GGT | TTC | GAC | TGG | GTC | TAC | TAT | 528 |
| | Met | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | Tyr | Tyr | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| | GAA | TCC | AAA | GCT | CAC | ATC | CAC | TGT | TCT | GTG | AAA | GCA | GAG | AAC | TCC | GTG | 576 |
| | Glu | Ser | Lys | Ala | His | Ile | His | Cys | Ser | Val | Lys | Ala | Glu | Asn | Ser | Val | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| 50 | GCG | GCC | AAA | TCC | GGC | GGC | TGT | TTC | CCG | GGA | TCC | GCC | ACC | GTG | CAC | CTG | 624 |
| | Ala | Ala | Lys | Ser | Gly | Gly | Cys | Phe | Pro | Gly | Ser | Ala | Thr | Val | His | Leu | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 55 | GAG | CAG | GGC | GGC | ACC | AAG | CTG | GTG | AAG | GAC | TTA | CGT | CCC | GGA | GAC | CGC | 672 |
| | Glu | Gln | Gly | Gly | Thr | Lys | Leu | Val | Lys | Asp | Leu | Arg | Pro | Gly | Asp | Arg | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| 60 | GTG | CTG | GCG | GCT | GAC | GAC | CAG | GGC | CGG | CTG | CTG | TAC | AGC | GAC | TTC | CTC | 720 |
| | Val | Leu | Ala | Ala | Asp | Asp | Gln | Gly | Arg | Leu | Leu | Tyr | Ser | Asp | Phe | Leu | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | ACC | TTC | CTG | GAC | CGC | GAC | GAA | GGC | GCC | AAG | AAG | GTC | TTC | TAC | GTG | ATC | 768 |
| | Thr | Phe | Leu | Asp | Arg | Asp | Glu | Gly | Ala | Lys | Lys | Val | Phe | Tyr | Val | Ile | |
| | | | | 245 | | | | | | 250 | | | | | 255 | | |
| 5 | GAG | ACG | CTG | GAG | CCG | CGC | GAG | CGC | CTG | CTG | CTC | ACC | GCC | GCG | CAC | CTG | 816 |
| | Glu | Thr | Leu | Glu | Pro | Arg | Glu | Arg | Leu | Leu | Leu | Thr | Ala | Ala | His | Leu | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | CTC | TTC | GTG | GCG | CCG | CAC | AAC | GAC | TCG | GGG | CCC | ACG | CCC | GGG | CCA | AGC | 864 |
| 10 | Leu | Phe | Val | Ala | Pro | His | Asn | Asp | Ser | Gly | Pro | Thr | Pro | Gly | Pro | Ser | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| | GCG | CTC | TTT | GCC | AGC | CGC | GTG | CGC | CCC | GGG | CAG | CGC | GTG | TAC | GTG | GTG | 912 |
| 15 | Ala | Leu | Phe | Ala | Ser | Arg | Val | Arg | Pro | Gly | Gln | Arg | Val | Tyr | Val | Val | |
| | | 290 | | | | | 295 | | | | 300 | | | | | | |
| | GCT | GAA | CGC | GGC | GGG | GAC | CGC | CGG | CTG | CTG | CCC | GCC | GCG | GTG | CAC | AGC | 960 |
| | Ala | Glu | Arg | Gly | Gly | Asp | Arg | Arg | Leu | Leu | Pro | Ala | Ala | Val | His | Ser | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 20 | GTG | ACG | CTG | CGA | GAG | GAG | GAG | GCG | GGC | GCG | TAC | GCG | CCG | CTC | ACG | GCG | 1008 |
| | Val | Thr | Leu | Arg | Glu | Glu | Glu | Ala | Gly | Ala | Tyr | Ala | Pro | Leu | Thr | Ala | |
| | | | | | 325 | | | | 330 | | | | | | 335 | | |
| 25 | CAC | GGC | ACC | ATT | CTC | ATC | AAC | CGG | GTG | CTC | GCC | TCG | TGC | TAC | GCT | GTC | 1056 |
| | His | Gly | Thr | Ile | Leu | Ile | Asn | Arg | Val | Leu | Ala | Ser | Cys | Tyr | Ala | Val | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| 30 | ATC | GAG | GAG | GAC | AGC | TGG | GCA | CAC | CGG | GCC | TTT | GCG | CCT | TTT | CGC | CTG | 1104 |
| | Ile | Glu | Glu | His | Ser | Trp | Ala | His | Arg | Ala | Phe | Ala | Pro | Phe | Arg | Leu | |
| | | | 355 | | | | 360 | | | | | | 365 | | | | |
| 35 | GCG | CAC | GCG | CTG | CTG | GCC | GCG | CTG | GCA | CCC | GCC | CGC | ACG | GAC | GGC | GGG | 1152 |
| | Ala | His | Ala | Leu | Leu | Ala | Ala | Leu | Ala | Pro | Ala | Arg | Thr | Asp | Gly | Gly | |
| | | 370 | | | | 375 | | | | | 380 | | | | | | |
| | GGC | GGG | GGC | AGC | ATC | CCT | GCA | GCG | CAA | TCT | GCA | ACG | GAA | GCG | AGG | GGC | 1200 |
| | Gly | Gly | Gly | Ser | Ile | Pro | Ala | Ala | Gln | Ser | Ala | Thr | Glu | Ala | Arg | Gly | |
| | 385 | | | | | 390 | | | | 395 | | | | | | 400 | |
| 40 | GCG | GAG | CCG | ACT | GCG | GGC | ATC | CAC | TGG | TAC | TCG | CAG | CTG | CTC | TAC | CAC | 1248 |
| | Ala | Glu | Pro | Thr | Ala | Gly | Ile | His | Trp | Tyr | Ser | Gln | Leu | Leu | Tyr | His | |
| | | | | | 405 | | | | 410 | | | | | | 415 | | |
| 45 | ATT | GGC | ACC | TGG | CTG | TTG | GAC | AGC | GAG | ACC | ATG | CAT | CCC | TTG | GGA | ATG | 1296 |
| | Ile | Gly | Thr | Trp | Leu | Leu | Asp | Ser | Glu | Thr | Met | His | Pro | Leu | Gly | Met | |
| | | | | 420 | | | | | 425 | | | | | 430 | | | |
| 50 | GCG | GTC | AAG | TCC | AGC | TG | | | | | | | | | | | 1313 |
| | Ala | Val | Lys | Ser | Ser | | | | | | | | | | | | |
| | | | 435 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1257

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | |
|----|---|-----|
| 10 | ATG CGG CTT TTG ACG AGA GTG CTG CTG GTG TCT CTT CTC ACT CTG TCC | 48 |
| | Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser | |
| | 1 5 10 15 | |
| 15 | TTG GTG GTG TCC GGA CTG GCC TGC GGT CCT GGC AGA GGC TAC GGC AGA | 96 |
| | Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg | |
| | 20 25 30 | |
| 20 | AGA AGA CAT CCG AAG AAG CTG ACA CCT CTC GCC TAC AAG CAG TTC ATA | 144 |
| | Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile | |
| | 35 40 45 | |
| 25 | CCT AAT GTC GCG GAG AAG ACC TTA GGG GCC AGC GGC AGA TAC GAG GGC | 192 |
| | Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly | |
| | 50 55 60 | |
| 30 | AAG ATA ACG CGC AAT TCG GAG AGA TTT AAA GAA CTT ACT CCA AAT TAC | 240 |
| | Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr | |
| | 65 70 75 80 | |
| 35 | AAT CCG GAG ATT ATC TTT AAG GAT GAG GAG AAC ACG GGA GCG GAC AGG | 288 |
| | Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg | |
| | 85 90 95 | |
| 40 | CTC ATG ACA CAG AGA TGC AAA GAC AAG CTG AAC TCG CTG GCC ATC TCT | 336 |
| | Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser | |
| | 100 105 110 | |
| 45 | GTA ATG AAC CAC TGG CCA GGG GTT AAG CTG CGT GTG ACA GAG GGC TGG | 384 |
| | Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp | |
| | 115 120 125 | |
| 50 | GAT GAG GAC GGT CAC CAT TTT GAA GAA TCA CTC CAC TAC GAG GGA AGA | 432 |
| | Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg | |
| | 130 135 140 | |
| 55 | GCT GTT GAT ATT ACC ACC TCT GAC CGA GAC AAG AGC AAA TAC GGG ACA | 480 |
| | Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr | |
| | 145 150 155 160 | |
| 60 | CTG TCT CGC CTA GCT GTG GAG GCT GGA TTT GAC TGG GTC TAT TAC GAG | 528 |
| | Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu | |
| | 165 170 175 | |
| 65 | TCC AAA GCC CAC ATT CAT TGC TCT GTC AAA GCA GAA AAT TCG GTT GCT | 576 |
| | Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala | |
| | 180 185 190 | |
| 70 | GCG AAA TCT GGG GGC TGT TTC CCA GGT TCG GCT CTG GTC TCG CTC CAG | 624 |
| | Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln | |
| | 195 200 205 | |
| 75 | GAC GGA GGA CAG AAG GCC GTG AAG GAC CTG AAC CCC GGA GAC AAG GTG | 672 |
| | Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val | |
| | 210 215 220 | |

| | | |
|----|---|------|
| 5 | CTG GCG GCA GAC AGC GCG GGA AAC CTG GTG TTC AGC GAC TTC ATC ATG Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met 225 230 235 240 | 720 |
| 10 | TTC ACA GAC CGA GAC TCC ACG ACG CGA CGT GTG TTT TAC GTC ATA GAA Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu 245 250 255 | 768 |
| 15 | ACG CAA GAA CCC GTT GAA AAG ATC ACC CTC ACC GCC GCT CAC CTC CTT Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu 260 265 270 | 816 |
| 20 | TTT GTC CTC GAC AAC TCA ACG GAA GAT CTC CAC ACC ATG ACC GCC GCG Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala 275 280 285 | 864 |
| 25 | TAT GCC AGC AGT GTC AGA GCC GGA CAA AAG GTG ATG GTT GTT GAT GAT Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp 290 295 300 | 912 |
| 30 | AGC GGT CAG CTT AAA TCT GTC ATC GTG CAG CGG ATA TAC ACG GAG GAG Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu 305 310 315 320 | 960 |
| 35 | CAG CGG GGC TCG TTC GCA CCA GTG ACT GCA CAT GGG ACC ATT GTG GTC Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val 325 330 335 | 1008 |
| 40 | GAC AGA ATA CTG GCG TCC TGT TAC GCC GTA ATA GAG GAC CAG GGG CTT Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu 340 345 350 | 1056 |
| 45 | GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser 355 360 365 | 1104 |
| 50 | TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn 370 375 380 | 1152 |
| 55 | AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr 385 390 395 400 | 1200 |
| 60 | TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn 405 410 415 | 1248 |
| 65 | TCA AGC TG Ser Ser | 1256 |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | |
|----|---|-----|
| 10 | ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG | 48 |
| | Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu | |
| | 1 5 10 15 | |
| 15 | CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG | 96 |
| | Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys | |
| | 20 25 30 | |
| 20 | AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC | 144 |
| | Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile | |
| | 35 40 45 | |
| 25 | CCC AAT GTG GCC GAG AAG ACC CTA GGC GCC AGC GGA AGG TAT GAA GGG | 192 |
| | Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly | |
| | 50 55 60 | |
| 30 | AAG ATC TCC AGA AAC TCC GAG CGA TTT AAG GAA CTC ACC CCC AAT TAC | 240 |
| | Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr | |
| | 65 70 75 80 | |
| 35 | AAC CCC GAC ATC ATA TTT AAG GAT GAA GAA AAC ACC GGA GCG GAC AGG | 288 |
| | Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg | |
| | 85 90 95 | |
| 40 | CTG ATG ACT CAG AGG TGT AAG GAC AAG TTG AAC GCT TTG GCC ATC TCG | 336 |
| | Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser | |
| | 100 105 110 | |
| 45 | GTG ATG AAC CAG TGG CCA GGA GTG AAA CTG CGG GTG ACC GAG GGC TGG | 384 |
| | Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp | |
| | 115 120 125 | |
| 50 | GAC GAA GAT GGC CAC CAC TCA GAG GAG TCT CTG CAC TAC GAG GGC CGC | 432 |
| | Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg | |
| | 130 135 140 | |
| 55 | GCA GTG GAC ATC ACC ACG TCT GAC CGC GAC CGC AGC AAG TAC GGC ATG | 480 |
| | Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met | |
| | 145 150 155 160 | |
| 60 | CTG GCC CGC CTG GCG GTG GAG GCC GGC TTC GAC TGG GTG TAC TAC GAG | 528 |
| | Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu | |
| | 165 170 175 | |
| 65 | TCC AAG GCA CAT ATC CAC TGC TCG GTG AAA GCA GAG AAC TCG GTG GCG | 576 |
| | Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala | |
| | 180 185 190 | |
| 70 | GCC AAA TCG GGA GGC TGC TTC CCG GGC TCG GCC ACG GTG CAC CTG GAG | 624 |
| | Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu | |
| | 195 200 205 | |
| 75 | CAG GGC GGC ACC AAG CTG GTG AAG GAC CTG AGC CCC GGG GAC CGC GTG | 672 |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Gln | Gly | Gly | Thr | Lys | Leu | Val | Lys | Asp | Leu | Ser | Pro | Gly | Asp | Arg | Val | |
| | 210 | | | | | | 215 | | | | | 220 | | | | | |
| 5 | CTG | GCG | GCG | GAC | GAC | CAG | GGC | CGG | CTG | CTC | TAC | AGC | GAC | TTC | CTC | ACT | 720 |
| | Leu | Ala | Ala | Asp | Asp | Gln | Gly | Arg | Leu | Leu | Tyr | Ser | Asp | Phe | Leu | Thr | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 10 | TTC | CTG | GAC | CGC | GAC | GAC | GGC | GCC | AAG | AAG | GTC | TTC | TAC | GTG | ATC | GAG | 768 |
| | Phe | Leu | Asp | Arg | Asp | Asp | Gly | Ala | Lys | Lys | Val | Phe | Tyr | Val | Ile | Glu | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 15 | ACG | CGG | GAG | CCG | CGC | GAG | CGC | CTG | CTG | CTC | ACC | GCC | GCG | CAC | CTG | CTC | 816 |
| | Thr | Arg | Glu | Pro | Arg | Glu | Arg | Leu | Leu | Leu | Thr | Ala | Ala | His | Leu | Leu | |
| | | | | 260 | | | | 265 | | | | | | 270 | | | |
| 20 | TTT | GTG | GCG | CCG | CAC | AAC | GAC | TCG | GCC | ACC | GGG | GAG | CCC | GAG | GCG | TCC | 864 |
| | Phe | Val | Ala | Pro | His | Asn | Asp | Ser | Ala | Thr | Gly | Glu | Pro | Glu | Ala | Ser | |
| | | 275 | | | | | 280 | | | | | | 285 | | | | |
| 25 | TCG | GGC | TCG | GGG | CCG | CCT | TCC | GGG | GGC | GCA | CTG | GGG | CCT | CGG | GCG | CTG | 912 |
| | Ser | Gly | Ser | Gly | Pro | Pro | Ser | Gly | Gly | Ala | Leu | Gly | Pro | Arg | Ala | Leu | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 30 | TTC | GCC | AGC | CGC | GTG | CGC | CCG | GGC | CAG | CGC | GTG | TAC | GTG | GTG | GCC | GAG | 960 |
| | Phe | Ala | Ser | Arg | Val | Arg | Pro | Gly | Gln | Arg | Val | Tyr | Val | Val | Ala | Glu | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 35 | CGT | GAC | GGG | GAC | CGC | CGG | CTC | CTG | CCC | GCC | GCT | GTG | CAC | AGC | GTG | ACC | 1008 |
| | Arg | Asp | Gly | Asp | Arg | Arg | Leu | Leu | Pro | Ala | Ala | Val | His | Ser | Val | Thr | |
| | | | | | 325 | | | | 330 | | | | | | 335 | | |
| 40 | CTA | AGC | GAG | GAG | GCC | GCG | GGC | GCC | TAC | GCG | CCG | CTC | ACG | GCC | CAG | GGC | 1056 |
| | Leu | Ser | Glu | Glu | Ala | Ala | Gly | Ala | Tyr | Ala | Pro | Leu | Thr | Ala | Gln | Gly | |
| | | | | 340 | | | | 345 | | | | | | 350 | | | |
| 45 | ACC | ATT | CTC | ATC | AAC | CGG | GTG | CTG | GCC | TCG | TGC | TAC | GCG | GTC | ATC | GAG | 1104 |
| | Thr | Ile | Leu | Ile | Asn | Arg | Val | Leu | Ala | Ser | Cys | Tyr | Ala | Val | Ile | Glu | |
| | | 355 | | | | | 360 | | | | | | 365 | | | | |
| 50 | GAG | CAC | AGC | TGG | GCG | CAC | CGG | GCC | TTC | GCG | CCC | TTC | CGC | CTG | GCG | CAC | 1152 |
| | Glu | His | Ser | Trp | Ala | His | Arg | Ala | Phe | Ala | Pro | Phe | Arg | Leu | Ala | His | |
| | | 370 | | | | | 375 | | | | | 380 | | | | | |
| 55 | GCG | CTC | CTG | GCT | GCA | CTG | GCG | CCC | GCG | CGC | ACG | GAC | CGC | GGC | GGG | GAC | 1200 |
| | Ala | Leu | Leu | Ala | Ala | Leu | Ala | Pro | Ala | Arg | Thr | Asp | Arg | Gly | Gly | Asp | |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| 60 | AGC | GGC | GGC | GGG | GAC | CGC | GGG | GGC | GGC | GGC | AGA | GTA | GCC | CTA | ACC | | 1248 |
| | Ser | Gly | Gly | Gly | Asp | Arg | Gly | Gly | Gly | Gly | Arg | Val | Ala | Leu | Thr | | |
| | | | | | 405 | | | 410 | | | | | | 415 | | | |
| 65 | GCT | CCA | GGT | GCT | GCC | GAC | GCT | CCG | GGT | GCG | GGG | GCC | ACC | GCG | GGC | ATC | 1296 |
| | Ala | Pro | Gly | Ala | Ala | Asp | Ala | Pro | Gly | Ala | Gly | Ala | Thr | Ala | Gly | Ile | |
| | | | | 420 | | | | 425 | | | | | | 430 | | | |
| 70 | CAC | TGG | TAC | TCG | CAG | CTG | CTC | TAC | CAA | ATA | GGC | ACC | TGG | CTC | CTG | GAC | 1344 |
| | His | Trp | Tyr | Ser | Gln | Leu | Leu | Tyr | Gln | Ile | Gly | Thr | Trp | Leu | Leu | Asp | |
| | | 435 | | | | | 440 | | | | | | 445 | | | | |
| 75 | AGC | GAG | GCC | CTG | CAC | CCG | CTG | GGC | ATG | GCG | GTC | AAG | TCC | AGC | NNN | AGC | 1392 |
| | Ser | Glu | Ala | Leu | His | Pro | Leu | Gly | Met | Ala | Val | Lys | Ser | Ser | Xaa | Ser | |

| | | | | |
|----------------------------------|--|-----|---------|------|
| | 450 | 455 | 460 | |
| | CGG GGG GCC GGG GGA GGG GCG CGG GAG GGG GCC | | | 1425 |
| 5 | Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala | | | |
| | 465 | 470 | 475 | |
| | | | | |
| (2) INFORMATION FOR SEQ ID NO:7: | | | | |
| 10 | (i) SEQUENCE CHARACTERISTICS: | | | |
| | (A) LENGTH: 1622 base pairs | | | |
| | (B) TYPE: nucleic acid | | | |
| | (C) STRANDEDNESS: both | | | |
| 15 | (D) TOPOLOGY: linear | | | |
| | (ii) MOLECULE TYPE: cDNA | | | |
| | (ix) FEATURE: | | | |
| 20 | (A) NAME/KEY: CDS | | | |
| | (B) LOCATION: 51..1283 | | | |
| | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: | | | |
| 25 | CATCAGCCCA CCAGGAGACC TCGCCC GCCG CTCCCCCGGG CTCCCCCGGCC ATG TCT | | | 56 |
| | | | Met Ser | |
| | | | 1 | |
| 30 | CCC GCC CGG CTC CGG CCC CGA CTG CAC TTC TGC CTG GTC CTG TTG CTG | | | 104 |
| | Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu | | | |
| | 5 | 10 | 15 | |
| 35 | CTG CTG GTG GTG CCC GCG GCA TGG GGC TGC GGG CCG GGT CGG GTG GTG | | | 152 |
| | Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val | | | |
| | 20 | 25 | 30 | |
| 40 | GGC AGC CGC CGG CGA CCG CCA CGC AAA CTC GTG CCG CTC GCC TAC AAG | | | 200 |
| | Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys | | | |
| | 35 | 40 | 45 | 50 |
| 45 | CAG TTC AGC CCC AAT GTG CCC GAG AAG ACC CTG GGC GCC AGC GGA CGC | | | 248 |
| | Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg | | | |
| | 55 | 60 | 65 | |
| 50 | TAT GAA GGC AAG ATC GCT CGC AGC TCC GAG CGC TTC AAG GAG CTC ACC | | | 296 |
| | Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr | | | |
| | 70 | 75 | 80 | |
| 55 | CCC AAT TAC AAT CCA GAC ATC ATC TTC AAG GAC GAG GAG AAC ACA GGC | | | 344 |
| | Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly | | | |
| | 85 | 90 | 95 | |
| 60 | GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGC CTG AAC TCG CTG | | | 392 |
| | Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu | | | |
| | 100 | 105 | 110 | |
| 65 | GCT ATC TCG GTG ATG AAC CAG TGG CCC GGT GTG AAG CTG CGG GTG ACC | | | 440 |
| | Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr | | | |
| | 115 | 120 | 125 | 130 |
| 70 | GAG GGC TGG GAC GAG GAC GGC CAC CAC TCA GAG GAG TCC CTG CAT TAT | | | 488 |
| | Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr | | | |
| | 135 | 140 | 145 | |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | GAG | GGC | CGC | GCG | GTG | GAC | ATC | ACC | ACA | TCA | GAC | CGC | GAC | CGC | AAT | AAG | 536 |
| | Glu | Gly | Arg | Ala | Val | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | Asn | Lys | |
| | | | | 150 | | | | | 155 | | | | | 160 | | | |
| 5 | TAT | GGA | CTG | CTG | GCG | CGC | TTG | GCA | GTG | GAG | GCC | GGC | TTT | GAC | TGG | GTG | 584 |
| | Tyr | Gly | Leu | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | |
| | | | 165 | | | | | 170 | | | | | 175 | | | | |
| 10 | TAT | TAC | GAG | TCA | AAG | GCC | CAC | GTG | CAT | TGC | TCC | GTC | AAG | TCC | GAG | CAC | 632 |
| | Tyr | Tyr | Glu | Ser | Lys | Ala | His | Val | His | Cys | Ser | Val | Lys | Ser | Glu | His | |
| | | 180 | | | | | 185 | | | | | 190 | | | | | |
| 15 | TCG | GCC | GCA | GCC | AAG | ACG | GGC | GGC | TGC | TTC | CCT | GCC | GGA | GCC | CAG | GTA | 680 |
| | Ser | Ala | Ala | Ala | Lys | Thr | Gly | Gly | Cys | Phe | Pro | Ala | Gly | Ala | Gln | Val | |
| | 195 | | | | | 200 | | | | | 205 | | | | 210 | | |
| 20 | CGC | CTG | GAG | AGT | GGG | GCG | CGT | GTG | GCC | TTG | TCA | GCC | GTG | AGG | CCG | GGA | 728 |
| | Arg | Leu | Glu | Ser | Gly | Ala | Arg | Val | Ala | Leu | Ser | Ala | Val | Arg | Pro | Gly | |
| | | | | 215 | | | | | | 220 | | | | | 225 | | |
| 25 | GAC | CGT | GTG | CTG | GCC | ATG | GGG | GAG | GAT | GGG | AGC | CCC | ACC | TTC | AGC | GAT | 776 |
| | Asp | Arg | Val | Leu | Ala | Met | Gly | Glu | Asp | Gly | Ser | Pro | Thr | Phe | Ser | Asp | |
| | | | | 230 | | | | 235 | | | | | | 240 | | | |
| 30 | GTG | CTC | ATT | TTC | CTG | GAC | CGC | GAG | CCC | CAC | AGG | CTG | AGA | GCC | TTC | CAG | 824 |
| | Val | Leu | Ile | Phe | Leu | Asp | Arg | Glu | Pro | His | Arg | Leu | Arg | Ala | Phe | Gln | |
| | | | 245 | | | | | 250 | | | | | 255 | | | | |
| 35 | GTC | ATC | GAG | ACT | CAG | GAC | CCC | CCA | CGC | CGC | CTG | GCA | CTC | ACA | CCC | GCT | 872 |
| | Val | Ile | Glu | Thr | Gln | Asp | Pro | Pro | Arg | Arg | Leu | Ala | Leu | Thr | Pro | Ala | |
| | | 260 | | | | | 265 | | | | | 270 | | | | | |
| 40 | CAC | CTG | CTC | TTT | ACG | GCT | GAC | AAT | CAC | ACG | GAG | CCG | GCA | GCC | CGC | TTC | 920 |
| | His | Leu | Leu | Phe | Thr | Ala | Asp | Asn | His | Thr | Glu | Pro | Ala | Ala | Arg | Phe | |
| | 275 | | | | | 280 | | | | | 285 | | | | 290 | | |
| 45 | CGG | GCC | ACA | TTT | GCC | AGC | CAC | GTG | CAG | CCT | GGC | CAG | TAC | GTG | CTG | GTG | 968 |
| | Arg | Ala | Thr | Phe | Ala | Ser | His | Val | Gln | Pro | Gly | Gln | Tyr | Val | Leu | Val | |
| | | | | 295 | | | | | | 300 | | | | | 305 | | |
| 50 | GCT | GGG | GTG | CCA | GGC | CTG | CAG | CCT | GCC | CGC | GTG | GCA | GCT | GTC | TCT | ACA | 1016 |
| | Ala | Gly | Val | Pro | Gly | Leu | Gln | Pro | Ala | Arg | Val | Ala | Ala | Val | Ser | Thr | |
| | | | 310 | | | | | 315 | | | | | | 320 | | | |
| 55 | CAC | GTG | GCC | CTC | GGG | GCC | TAC | GCC | CCG | CTC | ACA | AAG | CAT | GGG | ACA | CTG | 1064 |
| | His | Val | Ala | Leu | Gly | Ala | Tyr | Ala | Pro | Leu | Thr | Lys | His | Gly | Thr | Leu | |
| | | 325 | | | | | 330 | | | | | 335 | | | | | |
| 60 | GTG | GTG | GAG | GAT | GTG | GTG | GCA | TCC | TGC | TTC | GCG | GCC | GTG | GCT | GAC | CAC | 1112 |
| | Val | Val | Glu | Asp | Val | Val | Ala | Ser | Cys | Phe | Ala | Ala | Val | Ala | Asp | His | |
| | | 340 | | | | | 345 | | | | | 350 | | | | | |
| 65 | CAC | CTG | GCT | CAG | TTG | GCC | TTC | TGG | CCC | CTG | AGA | CTC | TTT | CAC | AGC | TTG | 1160 |
| | His | Leu | Ala | Gln | Leu | Ala | Phe | Trp | Pro | Leu | Arg | Leu | Phe | His | Ser | Leu | |
| | 355 | | | | 360 | | | | | | 365 | | | | | 370 | |
| 70 | GCA | TGG | GGC | AGC | TGG | ACC | CCG | GGG | GAG | GGT | GTG | CAT | TGG | TAC | CCC | CAG | 1208 |
| | Ala | Trp | Gly | Ser | Trp | Thr | Pro | Gly | Glu | Gly | Val | His | Trp | Tyr | Pro | Gln | |
| | | | | 375 | | | | | | 380 | | | | | 385 | | |

CTG CTC TAC CGC CTG GGG CGT CTC CTG CTA GAA GAG GGC AGC TTC CAC 1256
Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His
390 395 400

5 CCA CTG GGC ATG TCC GGG GCA GGG AGC TGAAAGGACT CCACCGCTGC 1303
Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410

10 CCTCCTGGAA CTGCTGTACT GGGTCCAGAA GCCTCTCAGC CAGGAGGGAG CTGGCCCTGG 1363

AAGGGACCTG AGCTGGGGGA CACTGGCTCC TGCCATCTCC TCTGCCATGA AGATACACCA 1423

TTGAGACTTG ACTGGGCAAC ACCAGCGTCC CCCACCCGCG TCGTGGTGTA GTCATAGAGC 1483

15 TGCAAGCTGA GCTGGCGAGG GGATGGTTGT TGACCCCTCT CTCCTAGAGA CCTTGAGGCT 1543

GGCACGGCGA CTCCCAACTC AGCCTGCTCT CACTACGAGT TTTCATACTC TGCCTCCCCC 1603

20 ATTGGGAGGG CCCATTCCC 1622

(2) INFORMATION FOR SEQ ID NO:8:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1191

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

40 ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG 48
Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15

45 GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG 96
Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30

CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT 144
Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45

50 GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG 192
Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60

55 GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC 240
Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
65 70 75 80

60 TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC 288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
85 90 95

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | CGC | CTG | ATG | ACC | GAG | CGT | TGC | AAG | GAG | AGG | GTG | AAC | GCT | TTG | GCC | ATT | 336 |
| | Arg | Leu | Met | Thr | Glu | Arg | Cys | Lys | Glu | Arg | Val | Asn | Ala | Leu | Ala | Ile | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| 5 | GCC | GTG | ATG | AAC | ATG | TGG | CCC | GGA | GTG | CGC | CTA | CGA | GTG | ACT | GAG | GGC | 384 |
| | Ala | Val | Met | Asn | Met | Trp | Pro | Gly | Val | Arg | Leu | Arg | Val | Thr | Glu | Gly | |
| | | | | 115 | | | | 120 | | | | | 125 | | | | |
| 10 | TGG | GAC | GAG | GAC | GGC | CAC | CAC | GCT | CAG | GAT | TCA | CTC | CAC | TAC | GAA | GGC | 432 |
| | Trp | Asp | Glu | Asp | Gly | His | His | Ala | Gln | Asp | Ser | Leu | His | Tyr | Glu | Gly | |
| | | 130 | | | | | | 135 | | | | 140 | | | | | |
| 15 | CGT | GCT | TTG | GAC | ATC | ACT | ACG | TCT | GAC | CGC | GAC | CGC | AAC | AAG | TAT | GGG | 480 |
| | Arg | Ala | Leu | Asp | Ile | Thr | Ser | Asp | Arg | Asp | Arg | Asn | Lys | Tyr | Gly | | |
| | 145 | | | | | 150 | | | | 155 | | | | | 160 | | |
| 20 | TTG | CTG | GCG | CGC | CTC | GCA | GTG | GAA | GCC | GGC | TTC | GAC | TGG | GTC | TAC | TAC | 528 |
| | Leu | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | Tyr | Tyr | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 25 | GAG | TCC | CGC | AAC | CAC | GTC | CAC | GTG | TCG | GTC | AAA | GCT | GAT | AAC | TCA | CTG | 576 |
| | Glu | Ser | Arg | Asn | His | Val | His | Val | Ser | Val | Lys | Ala | Asp | Asn | Ser | Leu | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 30 | GCG | GTC | CGG | GCG | GGC | GGC | TGC | TTT | CCG | GGA | AAT | GCA | ACT | GTG | CGC | CTG | 624 |
| | Ala | Val | Arg | Ala | Gly | Gly | Cys | Phe | Pro | Gly | Asn | Ala | Thr | Val | Arg | Leu | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 35 | TGG | AGC | GGC | GAG | CGG | AAA | GGG | CTG | CGG | GAA | CTG | CAC | CGC | GGA | GAC | TGG | 672 |
| | Trp | Ser | Gly | Glu | Arg | Lys | Gly | Leu | Arg | Glu | Leu | His | Arg | Gly | Asp | Trp | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| 40 | GTT | TTG | GCG | GCC | GAT | GCG | TCA | GGC | CGG | GTG | GTG | CCC | ACG | CCG | GTG | CTG | 720 |
| | Val | Leu | Ala | Ala | Asp | Ala | Ser | Gly | Arg | Val | Val | Pro | Thr | Pro | Val | Leu | |
| | 225 | | | | | 230 | | | | 235 | | | | | | 240 | |
| 45 | CTC | TTC | CTG | GAC | CGG | GAC | TTG | CAG | CGC | CGG | GCT | TCA | TTT | GTG | GCT | GTG | 768 |
| | Leu | Phe | Leu | Asp | Arg | Asp | Leu | Gln | Arg | Arg | Ala | Ser | Phe | Val | Ala | Val | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 50 | GAG | ACC | GAG | TGG | CCT | CCA | CGC | AAA | CTG | TTG | CTC | ACG | CCC | TGG | CAC | CTG | 816 |
| | Glu | Thr | Glu | Trp | Pro | Pro | Arg | Lys | Leu | Leu | Leu | Thr | Pro | Trp | His | Leu | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 55 | GTG | TTT | GCC | GCT | CGA | GGG | CCG | GCG | CCC | GCG | CCA | GGC | GAC | TTT | GCA | CCG | 864 |
| | Val | Phe | Ala | Ala | Arg | Gly | Pro | Ala | Pro | Ala | Pro | Gly | Asp | Phe | Ala | Pro | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 60 | GTG | TTC | GCG | CGC | CGG | CTA | CGC | GCT | GGG | GAC | TCG | GTG | CTG | GCG | CCC | GGC | 912 |
| | Val | Phe | Ala | Arg | Arg | Leu | Arg | Ala | Gly | Asp | Ser | Val | Leu | Ala | Pro | Gly | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 65 | GGG | GAT | GCG | CTT | CGG | CCA | GCG | CGC | GTG | GCC | CGT | GTG | GCG | CGG | GAG | GAA | 960 |
| | Gly | Asp | Ala | Leu | Arg | Pro | Ala | Arg | Val | Ala | Arg | Val | Ala | Arg | Glu | Glu | |
| | 305 | | | | | 310 | | | | 315 | | | | | 320 | | |
| 70 | GCC | GTG | GGC | GTG | TTC | GCG | CCG | CTC | ACC | GCG | CAC | GGG | ACG | CTG | CTG | GTG | 1008 |
| | Ala | Val | Gly | Val | Phe | Ala | Pro | Leu | Thr | Ala | His | Gly | Thr | Leu | Leu | Val | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 75 | AAC | GAT | GTC | CTG | GCC | TCT | TGC | TAC | GCG | GTT | CTG | GAG | AGT | CAC | CAG | TGG | 1056 |
| | Asn | Asp | Val | Leu | Ala | Ser | Cys | Tyr | Ala | Val | Leu | Glu | Ser | His | Gln | Trp | |

| | | | | | | |
|----|--|-----|-----|------|----|-----|
| | 340 | 345 | 350 | | | |
| 5 | GCG CAC CGC GCT TTT GCC CCC TTG AGA CTG CTG CAC GCG CTA GGG GCG Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala | 360 | 365 | 1104 | | |
| 10 | CTG CTC CCC GGC GGG GCC GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser | 370 | 380 | 1152 | | |
| 15 | CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC TGA Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly | 385 | 395 | 1191 | | |
| 20 | (2) INFORMATION FOR SEQ ID NO:9: | | | | | |
| 25 | (i) SEQUENCE CHARACTERISTICS: | | | | | |
| | (A) LENGTH: 1251 base pairs | | | | | |
| | (B) TYPE: nucleic acid | | | | | |
| | (C) STRANDEDNESS: both | | | | | |
| | (D) TOPOLOGY: linear | | | | | |
| 30 | (ii) MOLECULE TYPE: cDNA | | | | | |
| | (ix) FEATURE: | | | | | |
| | (A) NAME/KEY: CDS | | | | | |
| | (B) LOCATION: 1..1248 | | | | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: | | | | | |
| 40 | ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile | 1 | 5 | 10 | 15 | 48 |
| 45 | AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly | 20 | 25 | 30 | | 96 |
| 50 | TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys | 35 | 40 | 45 | | 144 |
| 55 | CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys | 50 | 55 | 60 | | 192 |
| 60 | TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile | 65 | 70 | 75 | 80 | 240 |
| | CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn | 85 | 90 | 95 | | 288 |
| | GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu | 100 | 105 | 110 | | 336 |
| | GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT | | | | | 384 |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Ala | Ile | Ser | Val | Met | Asn | His | Trp | Pro | Gly | Val | Lys | Leu | Arg | Val | Thr | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 5 | GAA | GGC | TGG | GAT | GAG | GAT | GGT | CAC | CAT | TTA | GAA | GAA | TCT | TTG | CAC | TAT | 432 |
| | Glu | Gly | Trp | Asp | Glu | Asp | Gly | His | His | Leu | Glu | Glu | Ser | Leu | His | Tyr | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| 10 | GAG | GGA | CGG | GCA | GTG | GAC | ATC | ACT | ACC | TCA | GAC | AGG | GAT | AAA | AGC | AAG | 480 |
| | Glu | Gly | Arg | Ala | Val | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Lys | Ser | Lys | |
| | | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| 15 | TAT | GGG | ATG | CTA | TCC | AGG | CTT | GCA | GTG | GAG | GCA | GGA | TTC | GAC | TGG | GTC | 528 |
| | Tyr | Gly | Met | Leu | Ser | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 20 | TAT | TAT | GAA | TCT | AAA | GCC | CAC | ATA | CAC | TGC | TCT | GTC | AAA | GCA | GAA | AAT | 576 |
| | Tyr | Tyr | Glu | Ser | Lys | Ala | His | Ile | His | Cys | Ser | Val | Lys | Ala | Glu | Asn | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 25 | TCA | GTG | GCT | GCT | AAA | TCA | GGA | GGA | TGT | TTT | CCT | GGG | TCT | GGG | ACG | GTG | 624 |
| | Ser | Val | Ala | Ala | Lys | Ser | Gly | Gly | Cys | Phe | Pro | Gly | Ser | Gly | Thr | Val | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 30 | ACA | CTT | GGT | GAT | GGG | ACG | AGG | AAA | CCC | ATC | AAA | GAT | CTT | AAA | GTG | GGC | 672 |
| | Thr | Leu | Gly | Asp | Gly | Thr | Arg | Lys | Pro | Ile | Lys | Asp | Leu | Lys | Val | Gly | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| 35 | GAC | CGG | GTT | TTG | GCT | GCA | GAC | GAG | AAG | GGA | AAT | GTC | TTA | ATA | AGC | GAC | 720 |
| | Asp | Arg | Val | Leu | Ala | Ala | Asp | Glu | Lys | Gly | Asn | Val | Leu | Ile | Ser | Asp | |
| | | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| 40 | TTT | ATT | ATG | TTT | ATA | GAC | CAC | GAT | CCG | ACA | ACG | AGA | AGG | CAA | TTC | ATC | 768 |
| | Phe | Ile | Met | Phe | Ile | Asp | His | Asp | Pro | Thr | Thr | Arg | Arg | Gln | Phe | Ile | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 45 | GTC | ATC | GAG | ACG | TCA | GAA | CCT | TTC | ACC | AAG | CTC | ACC | CTC | ACT | GCC | GCG | 816 |
| | Val | Ile | Glu | Thr | Ser | Glu | Pro | Phe | Thr | Lys | Leu | Thr | Leu | Thr | Ala | Ala | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 50 | CAC | CTA | GTT | TTC | GTT | GGA | AAC | TCT | TCA | GCA | GCT | TCG | GGT | ATA | ACA | GCA | 864 |
| | His | Leu | Val | Phe | Val | Gly | Asn | Ser | Ser | Ala | Ala | Ser | Gly | Ile | Thr | Ala | |
| | | | 275 | | | | 280 | | | | | | 285 | | | | |
| 55 | ACA | TTT | GCC | AGC | AAC | GTG | AAG | CCT | GGA | GAT | ACA | GTT | TTA | GTG | TGG | GAA | 912 |
| | Thr | Phe | Ala | Ser | Asn | Val | Lys | Pro | Gly | Asp | Thr | Val | Leu | Val | Trp | Glu | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 60 | GAC | ACA | TGC | GAG | AGC | CTC | AAG | AGC | GTT | ACA | GTG | AAA | AGG | ATT | TAC | ACT | 960 |
| | Asp | Thr | Cys | Glu | Ser | Leu | Lys | Ser | Val | Thr | Val | Lys | Arg | Ile | Tyr | Thr | |
| | | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| 65 | GAG | GAG | CAC | GAG | GGC | TCT | TTT | GCG | CCA | GTC | ACC | GCG | CAC | GGA | ACC | ATA | 1008 |
| | Glu | Glu | His | Glu | Gly | Ser | Phe | Ala | Pro | Val | Thr | Ala | His | Gly | Thr | Ile | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 70 | ATA | GTG | GAT | CAG | GTG | TTG | GCA | TCG | TGC | TAC | GCG | GTC | ATT | GAG | AAC | CAC | 1056 |
| | Ile | Val | Asp | Gln | Val | Leu | Ala | Ser | Cys | Tyr | Ala | Val | Ile | Glu | Asn | His | |
| | | | | 340 | | | | 345 | | | | | | 350 | | | |
| 75 | AAA | TGG | GCA | CAT | TGG | GCT | TTT | GCG | CCG | GTC | AGG | TTG | TGT | CAC | AAG | CTG | 1104 |
| | Lys | Trp | Ala | His | Trp | Ala | Phe | Ala | Pro | Val | Arg | Leu | Cys | His | Lys | Leu | |

| | 355 | 360 | 365 | |
|----|---|-----|-----|------|
| 5 | ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu 370 375 380 | | | 1152 |
| 10 | GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp 385 390 395 400 | | | 1200 |
| | CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser 405 410 415 | | | 1248 |
| 15 | TGA | | | 1251 |

(2) INFORMATION FOR SEQ ID NO:10:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | |
|----|--|
| 30 | Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile 1 5 10 15 |
| 35 | Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly 20 25 30 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys 35 40 45 |
| 40 | Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg 50 55 60 |
| 45 | Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr 65 70 75 80 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly 85 90 95 |
| 50 | Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu 100 105 110 |
| 55 | Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr 115 120 125 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr 130 135 140 |
| 60 | Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys 145 150 155 160 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val 165 170 175 |

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190
 5 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
 195 200 205
 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
 210 215 220
 10 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
 225 230 235 240
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
 245 250 255
 15 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
 260 265 270
 20 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
 275 280 285
 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
 290 295 300
 25 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
 305 310 315 320
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
 325 330 335
 30 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
 340 345 350
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365
 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380
 40 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
 385 390 395 400
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415
 45 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425

50 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu

| | 1 | | 5 | | 10 | | 15 | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Ala | Leu | Ser | Ala | Gln | Ser | Cys | Gly | Pro | Gly | Arg | Gly | Pro | Val | Gly | Arg |
| | | | | 20 | | | | | 25 | | | | | 30 | | |
| 5 | Arg | Arg | Tyr | Val | Arg | Lys | Gln | Leu | Val | Pro | Leu | Leu | Tyr | Lys | Gln | Phe |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| | Val | Pro | Ser | Met | Pro | Glu | Arg | Thr | Leu | Gly | Ala | Ser | Gly | Pro | Ala | Glu |
| 10 | | 50 | | | | | 55 | | | | | 60 | | | | |
| | Gly | Arg | Val | Thr | Arg | Gly | Ser | Glu | Arg | Phe | Arg | Asp | Leu | Val | Pro | Asn |
| | 65 | | | | | 70 | | | | 75 | | | | | | 80 |
| 15 | Tyr | Asn | Pro | Asp | Ile | Ile | Phe | Lys | Asp | Glu | Glu | Asn | Ser | Gly | Ala | Asp |
| | | | | | 85 | | | | | 90 | | | | | 95 | |
| | Arg | Leu | Met | Thr | Glu | Arg | Cys | Lys | Glu | Arg | Val | Asn | Ala | Leu | Ala | Ile |
| 20 | | | | 100 | | | | | 105 | | | | | 110 | | |
| | Ala | Val | Met | Asn | Met | Trp | Pro | Gly | Val | Arg | Leu | Arg | Val | Thr | Glu | Gly |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| 25 | Trp | Asp | Glu | Asp | Gly | His | His | Ala | Gln | Asp | Ser | Leu | His | Tyr | Glu | Gly |
| | 130 | | | | | 135 | | | | | | 140 | | | | |
| | Arg | Ala | Leu | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | Asn | Lys | Tyr | Gly |
| | 145 | | | | 150 | | | | | 155 | | | | | | 160 |
| 30 | Leu | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | Tyr | Tyr |
| | | | | | 165 | | | | | 170 | | | | | 175 | |
| | Glu | Ser | Arg | Asn | His | Ile | His | Val | Ser | Val | Lys | Ala | Asp | Asn | Ser | Leu |
| 35 | | | | 180 | | | | | 185 | | | | | 190 | | |
| | Ala | Val | Arg | Ala | Gly | Gly | Cys | Phe | Pro | Gly | Asn | Ala | Thr | Val | Arg | Leu |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| 40 | Arg | Ser | Gly | Glu | Arg | Lys | Gly | Leu | Arg | Glu | Leu | His | Arg | Gly | Asp | Trp |
| | 210 | | | | | | 215 | | | | | 220 | | | | |
| | Val | Leu | Ala | Ala | Asp | Ala | Ala | Gly | Arg | Val | Val | Pro | Thr | Pro | Val | Leu |
| | 225 | | | | | 230 | | | | 235 | | | | | | 240 |
| 45 | Leu | Phe | Leu | Asp | Arg | Asp | Leu | Gln | Arg | Arg | Ala | Ser | Phe | Val | Ala | Val |
| | | | | 245 | | | | | 250 | | | | | | 255 | |
| | Glu | Thr | Glu | Arg | Pro | Pro | Arg | Lys | Leu | Leu | Leu | Thr | Pro | Trp | His | Leu |
| 50 | | | | 260 | | | | | 265 | | | | | 270 | | |
| | Val | Phe | Ala | Ala | Arg | Gly | Pro | Ala | Pro | Ala | Pro | Gly | Asp | Phe | Ala | Pro |
| | | | 275 | | | | | 280 | | | | | 285 | | | |
| 55 | Val | Phe | Ala | Arg | Arg | Leu | Arg | Ala | Gly | Asp | Ser | Val | Leu | Ala | Pro | Gly |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| | Gly | Asp | Ala | Leu | Gln | Pro | Ala | Arg | Val | Ala | Arg | Val | Ala | Arg | Glu | Glu |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| 60 | Ala | Val | Gly | Val | Phe | Ala | Pro | Leu | Thr | Ala | His | Gly | Thr | Leu | Leu | Val |
| | | | | | 325 | | | | | 330 | | | | | 335 | |

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

5 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

10 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
385 390 395

(2) INFORMATION FOR SEQ ID NO:12:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30

30 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

35 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

40 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

45 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125

50 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160

55 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
180 185 190

60 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala

| | 195 | 200 | 205 |
|----|--|-----|-----|
| 5 | Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys 210 215 220 | | |
| | Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe 225 230 235 240 | | |
| 10 | Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala 245 250 255 | | |
| | Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr 260 265 270 | | |
| 15 | Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala 275 280 285 | | |
| | His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val 290 295 300 | | |
| 20 | Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val 305 310 315 320 | | |
| | Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly 325 330 335 | | |
| 25 | Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala 340 345 350 | | |
| 30 | Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro 355 360 365 | | |
| | Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr 370 375 380 | | |
| 35 | Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr 385 390 395 400 | | |
| 40 | Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410 | | |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | |
|----|--|
| 55 | Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser 1 5 10 15 |
| | Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly 20 25 30 |
| 60 | Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe |

| | 35 | 40 | 45 |
|----|--|----|----|
| 5 | Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu 50 55 60 | | |
| | Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn 65 70 75 80 | | |
| 10 | Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp 85 90 95 | | |
| | Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile 100 105 110 | | |
| 15 | Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly 115 120 125 | | |
| | Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly 130 135 140 | | |
| 20 | Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly 145 150 155 160 | | |
| | Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr 165 170 175 | | |
| 25 | Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val 180 185 190 | | |
| 30 | Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu 195 200 205 | | |
| | Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg 210 215 220 | | |
| 35 | Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu 225 230 235 240 | | |
| | Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile 245 250 255 | | |
| 40 | Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu 260 265 270 | | |
| 45 | Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser 275 280 285 | | |
| | Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val 290 295 300 | | |
| 50 | Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser 305 310 315 320 | | |
| | Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala 325 330 335 | | |
| 55 | His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val 340 345 350 | | |
| 60 | Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu 355 360 365 | | |

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
370 375 380

5 Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
405 410 415

10 Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
420 425 430

Ala Val Lys Ser Ser
435

15

(2) INFORMATION FOR SEQ ID NO:14:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

30 Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

35 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

40 Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

45 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

50 Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

55 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
145 150 155 160

60 Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190
 5 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
 195 200 205
 Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
 210 215 220
 10 Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
 225 230 235 240
 Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
 245 250 255
 15 Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
 260 265 270
 20 Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
 275 280 285
 Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
 290 295 300
 25 Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320
 Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335
 30 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350
 35 Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365
 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380
 40 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400
 Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415
 45 Ser Ser

50 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

60 Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu

| | 1 | | 5 | | 10 | | 15 | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Leu | Val | Cys | Ser | Gly | Leu | Ala | Cys | Gly | Pro | Gly | Arg | Gly | Phe | Gly | Lys |
| | | | 20 | | | | | | 25 | | | | | 30 | | |
| 5 | Arg | Arg | His | Pro | Lys | Lys | Leu | Thr | Pro | Leu | Ala | Tyr | Lys | Gln | Phe | Ile |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| 10 | Pro | Asn | Val | Ala | Glu | Lys | Thr | Leu | Gly | Ala | Ser | Gly | Arg | Tyr | Glu | Gly |
| | | 50 | | | | | 55 | | | | | 60 | | | | |
| | Lys | Ile | Ser | Arg | Asn | Ser | Glu | Arg | Phe | Lys | Glu | Leu | Thr | Pro | Asn | Tyr |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| 15 | Asn | Pro | Asp | Ile | Ile | Phe | Lys | Asp | Glu | Glu | Asn | Thr | Gly | Ala | Asp | Arg |
| | | | | | 85 | | | | | 90 | | | | | 95 | |
| | Leu | Met | Thr | Gln | Arg | Cys | Lys | Asp | Lys | Leu | Asn | Ala | Leu | Ala | Ile | Ser |
| | | | | 100 | | | | | 105 | | | | | 110 | | |
| 20 | Val | Met | Asn | Gln | Trp | Pro | Gly | Val | Lys | Leu | Arg | Val | Thr | Glu | Gly | Trp |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| | Asp | Glu | Asp | Gly | His | His | Ser | Glu | Glu | Ser | Leu | His | Tyr | Glu | Gly | Arg |
| | 130 | | | | | | 135 | | | | | 140 | | | | |
| 25 | Ala | Val | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | Ser | Lys | Tyr | Gly | Met |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| 30 | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | Tyr | Tyr | Glu |
| | | | | | 165 | | | | | 170 | | | | | 175 | |
| | Ser | Lys | Ala | His | Ile | His | Cys | Ser | Val | Lys | Ala | Glu | Asn | Ser | Val | Ala |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| 35 | Ala | Lys | Ser | Gly | Gly | Cys | Phe | Pro | Gly | Ser | Ala | Thr | Val | His | Leu | Glu |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| | Gln | Gly | Gly | Thr | Lys | Leu | Val | Lys | Asp | Leu | Ser | Pro | Gly | Asp | Arg | Val |
| | 210 | | | | | 215 | | | | | | 220 | | | | |
| 40 | Leu | Ala | Ala | Asp | Asp | Gln | Gly | Arg | Leu | Leu | Tyr | Ser | Asp | Phe | Leu | Thr |
| | 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| 45 | Phe | Leu | Asp | Arg | Asp | Asp | Gly | Ala | Lys | Lys | Val | Phe | Tyr | Val | Ile | Glu |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| | Thr | Arg | Glu | Pro | Arg | Glu | Arg | Leu | Leu | Leu | Thr | Ala | Ala | His | Leu | Leu |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| 50 | Phe | Val | Ala | Pro | His | Asn | Asp | Ser | Ala | Thr | Gly | Glu | Pro | Glu | Ala | Ser |
| | | | 275 | | | | | 280 | | | | | 285 | | | |
| | Ser | Gly | Ser | Gly | Pro | Pro | Ser | Gly | Gly | Ala | Leu | Gly | Pro | Arg | Ala | Leu |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| 55 | Phe | Ala | Ser | Arg | Val | Arg | Pro | Gly | Gln | Arg | Val | Tyr | Val | Val | Ala | Glu |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| 60 | Arg | Asp | Gly | Asp | Arg | Arg | Leu | Leu | Pro | Ala | Ala | Val | His | Ser | Val | Thr |
| | | | | | 325 | | | | | 330 | | | | | 335 | |

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
340 345 350

5 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
355 360 365

Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
370 375 380

10 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
385 390 395 400

15 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
405 410 415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
420 425 430

20 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
435 440 445

Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
450 455 460

25 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
465 470 475

(2) INFORMATION FOR SEQ ID NO:16:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

40 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
1 5 10 15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
20 25 30

45 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

50 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

55 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

60 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg

| | 115 | | 120 | | 125 |
|----|--|--|-----|--|-----|
| 5 | Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu 130 135 140 | | | | |
| | His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg 145 150 155 160 | | | | |
| 10 | Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp 165 170 175 | | | | |
| | Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser 180 185 190 | | | | |
| 15 | Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala 195 200 205 | | | | |
| | Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg 210 215 220 | | | | |
| 20 | Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe 225 230 235 240 | | | | |
| | Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala 245 250 255 | | | | |
| 25 | Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr 260 265 270 | | | | |
| 30 | Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala 275 280 285 | | | | |
| | Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val 290 295 300 | | | | |
| 35 | Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val 305 310 315 320 | | | | |
| | Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly 325 330 335 | | | | |
| 40 | Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala 340 345 350 | | | | |
| 45 | Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His 355 360 365 | | | | |
| | Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr 370 375 380 | | | | |
| 50 | Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser 385 390 395 400 | | | | |
| | Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410 | | | | |

(2) INFORMATION FOR SEQ ID NO:17:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Met | Ala | Leu | Leu | Thr | Asn | Leu | Leu | Pro | Leu | Cys | Cys | Leu | Ala | Leu | Leu | |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| 10 | Ala | Leu | Pro | Ala | Gln | Ser | Cys | Gly | Pro | Gly | Arg | Gly | Pro | Val | Gly | Arg | |
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| | Arg | Arg | Tyr | Ala | Arg | Lys | Gln | Leu | Val | Pro | Leu | Leu | Tyr | Lys | Gln | Phe | |
| | | | 35 | | | | | 40 | | | | | 45 | | | | |
| 15 | Val | Pro | Gly | Val | Pro | Glu | Arg | Thr | Leu | Gly | Ala | Ser | Gly | Pro | Ala | Glu | |
| | | 50 | | | | | 55 | | | | | 60 | | | | | |
| | Gly | Arg | Val | Ala | Arg | Gly | Ser | Glu | Arg | Phe | Arg | Asp | Leu | Val | Pro | Asn | |
| | 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| 20 | Tyr | Asn | Pro | Asp | Ile | Ile | Phe | Lys | Asp | Glu | Glu | Asn | Ser | Gly | Ala | Asp | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| | Arg | Leu | Met | Thr | Glu | Arg | Cys | Lys | Glu | Arg | Val | Asn | Ala | Leu | Ala | Ile | |
| 25 | | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Ala | Val | Met | Asn | Met | Trp | Pro | Gly | Val | Arg | Leu | Arg | Val | Thr | Glu | Gly | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 30 | Trp | Asp | Glu | Asp | Gly | His | His | Ala | Gln | Asp | Ser | Leu | His | Tyr | Glu | Gly | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| | Arg | Ala | Leu | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | Asn | Lys | Tyr | Gly | |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 35 | Leu | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | Tyr | Tyr | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| | Glu | Ser | Arg | Asn | His | Val | His | Val | Ser | Val | Lys | Ala | Asp | Asn | Ser | Leu | |
| 40 | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Ala | Val | Arg | Ala | Gly | Gly | Cys | Phe | Pro | Gly | Asn | Ala | Thr | Val | Arg | Leu | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 45 | Trp | Ser | Gly | Glu | Arg | Lys | Gly | Leu | Arg | Glu | Leu | His | Arg | Gly | Asp | Trp | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Val | Leu | Ala | Ala | Asp | Ala | Ser | Gly | Arg | Val | Val | Pro | Thr | Pro | Val | Leu | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 50 | Leu | Phe | Leu | Asp | Arg | Asp | Leu | Gln | Arg | Arg | Ala | Ser | Phe | Val | Ala | Val | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| | Glu | Thr | Glu | Trp | Pro | Pro | Arg | Lys | Leu | Leu | Leu | Thr | Pro | Trp | His | Leu | |
| 55 | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | Val | Phe | Ala | Ala | Arg | Gly | Pro | Ala | Pro | Ala | Pro | Gly | Asp | Phe | Ala | Pro | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 60 | Val | Phe | Ala | Arg | Arg | Leu | Arg | Ala | Gly | Asp | Ser | Val | Leu | Ala | Pro | Gly | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

5 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

10 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

15 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385 390 395

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
1 5 10 15

35 Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

40 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
50 55 60

45 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
85 90 95

50 Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

55 Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
130 135 140

60 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
145 150 155 160

Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175
 5 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190
 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
 195 200 205
 10 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
 210 215 220
 Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
 225 230 235 240
 15 Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
 245 250 255
 20 Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
 260 265 270
 His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
 275 280 285
 25 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
 290 295 300
 Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
 305 310 315 320
 30 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
 325 330 335
 35 Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
 340 345 350
 Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
 355 360 365
 40 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400
 45 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

50 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

60 (ix) FEATURE:
 (A) NAME/KEY: CDS

(B) LOCATION: 1..1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | | |
|----|---|-----|
| 5 | ATG GAT AAC CAC AGC TCA GTG CCT TGG GCC AGT GCC GCC AGT GTC ACC | 48 |
| | Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr | |
| | 1 5 10 15 | |
| 10 | TGT CTC TCC CTG GGA TGC CAA ATG CCA CAG TTC CAG TTC CAG TTC CAG | 96 |
| | Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln | |
| | 20 25 30 | |
| 15 | CTC CAA ATC CGC AGC GAG CTC CAT CTC CGC AAG CCC GCA AGA AGA ACG | 144 |
| | Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr | |
| | 35 40 45 | |
| 20 | CAA ACG ATG CGC CAC ATT GCG CAT ACG CAG CGT TGC CTC AGC AGG CTG | 192 |
| | Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu | |
| | 50 55 60 | |
| 25 | ACC TCT CTG GTG GCC CTG CTG CTG ATC GTC TTG CCG ATG GTC TTT AGC | 240 |
| | Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser | |
| | 65 70 75 80 | |
| 30 | CCG GCT CAC AGC TGC GGT CCT GGC CGA GGA TTG GGT CGT CAT AGG GCG | 288 |
| | Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala | |
| | 85 90 95 | |
| 35 | CGC AAC CTG TAT CCG CTG GTC CTC AAG CAG ACA ATT CCC AAT CTA TCC | 336 |
| | Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser | |
| | 100 105 110 | |
| 40 | GAG TAC ACG AAC AGC GCC TCC GGA CCT CTG GAG GGT GTG ATC CGT CGG | 384 |
| | Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg | |
| | 115 120 125 | |
| 45 | GAT TCG CCC AAA TTC AAG GAC CTC GTG CCC AAC TAC AAC AGG GAC ATC | 432 |
| | Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile | |
| | 130 135 140 | |
| 50 | CTT TTC CGT GAC GAG GAA GGC ACC GGA GCG GAT GGC TTG ATG AGC AAG | 480 |
| | Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys | |
| | 145 150 155 160 | |
| 55 | CGC TGC AAG GAG AAG CTA AAC GTG CTG GCC TAC TCG GTG ATG AAC GAA | 528 |
| | Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu | |
| | 165 170 175 | |
| 60 | TGG CCC GGC ATC CGG CTG CTG GTC ACC GAG AGC TGG GAC GAG GAC TAC | 576 |
| | Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr | |
| | 180 185 190 | |
| 65 | CAT CAC GGC CAG GAG TCG CTC CAC TAC GAG GGC CGA GCG GTG ACC ATT | 624 |
| | His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile | |
| | 195 200 205 | |
| 70 | GCC ACC TCC GAT CGC GAC CAG TCC AAA TAC GGC ATG CTC GCT CGC CTG | 672 |
| | Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu | |
| | 210 215 220 | |
| 75 | GCC GTC GAG GCT GGA TTC GAT TGG GTC TCC TAC GTC AGC AGG CGC CAC | 720 |

[illegible]

465

470

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
1 5 10 15
Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
20 25 30
Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
35 40 45
Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
50 55 60
Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
65 70 75 80
Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
85 90 95
Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
100 105 110
Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
115 120 125
Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
130 135 140
Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
145 150 155 160
Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
165 170 175
Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
180 185 190
His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
195 200 205
Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
210 215 220
Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
225 230 235 240
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
245 250 255

Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
260 265 270

5 Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
275 280 285

Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
290 295 300

10 Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
305 310 315 320

Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
325 330 335

15 Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
340 345 350

20 Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
355 360 365

Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
370 375 380

25 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
385 390 395 400

Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
405 410 415

30 Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
420 425 430

35 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
435 440 445

Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
450 455 460

40 Pro Gln Ser Trp Arg His Asp
465 470

45 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
1 5 10 15

60 Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr

| | 20 | 25 | 30 |
|----|------------------------------------|----------------------------|--------------------------------|
| 5 | Leu Gly Ala Ser Gly Arg Tyr 35 | Glu Gly Lys Ile Xaa 40 | Arg Asn Ser Glu 45 |
| | Arg Phe Lys Glu Leu Thr 50 | Pro Asn Tyr Asn Pro 55 | Asp Ile Ile Phe Lys 60 |
| 10 | Asp Glu Glu Asn Thr Gly Ala 65 | Asp Arg Leu Met Thr 70 | Gln Arg Cys Lys 75 80 |
| | Asp Lys Leu Asn Xaa Leu Ala 85 | Ile Ser Val Met Asn 90 | Xaa Trp Pro Gly 95 |
| 15 | Val Xaa Leu Arg Val Thr Glu 100 | Gly Trp Asp Glu Asp 105 | Gly His His Xaa 110 |
| | Glu Glu Ser Leu His Tyr Glu 115 | Gly Arg Ala Val Asp 120 | Ile Thr Thr Ser 125 |
| 20 | Asp Arg Asp Xaa Ser Lys Tyr 130 | Gly Xaa Leu Xaa Arg 135 | Leu Ala Val Glu 140 |
| | Ala Gly Phe Asp Trp Val Tyr 145 | Tyr Tyr Glu Ser Lys 150 | Ala His Ile His Cys 155 160 |
| 25 | Ser Val Lys Ala Glu Asn Ser 165 | Val Ala Ala Lys Ser 170 | Gly Gly Cys Phe 175 |
| | Pro Gly Ser Ala Xaa Val Xaa 180 | Leu Xaa Xaa Gly Gly 185 | Xaa Lys Xaa Val 190 |
| | Lys Asp Leu Xaa Pro Gly Asp 195 | Xaa Val Leu Ala Ala 200 | Asp Xaa Xaa Gly 205 |
| 35 | Xaa Leu Xaa Xaa Ser Asp Phe 210 | Xaa Xaa Phe Xaa Asp 215 | Arg 220 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| |
|--|
| Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys 1 5 10 15 |
| Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu 20 25 30 |
| Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa 35 40 45 |
| Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile |

[illegible]